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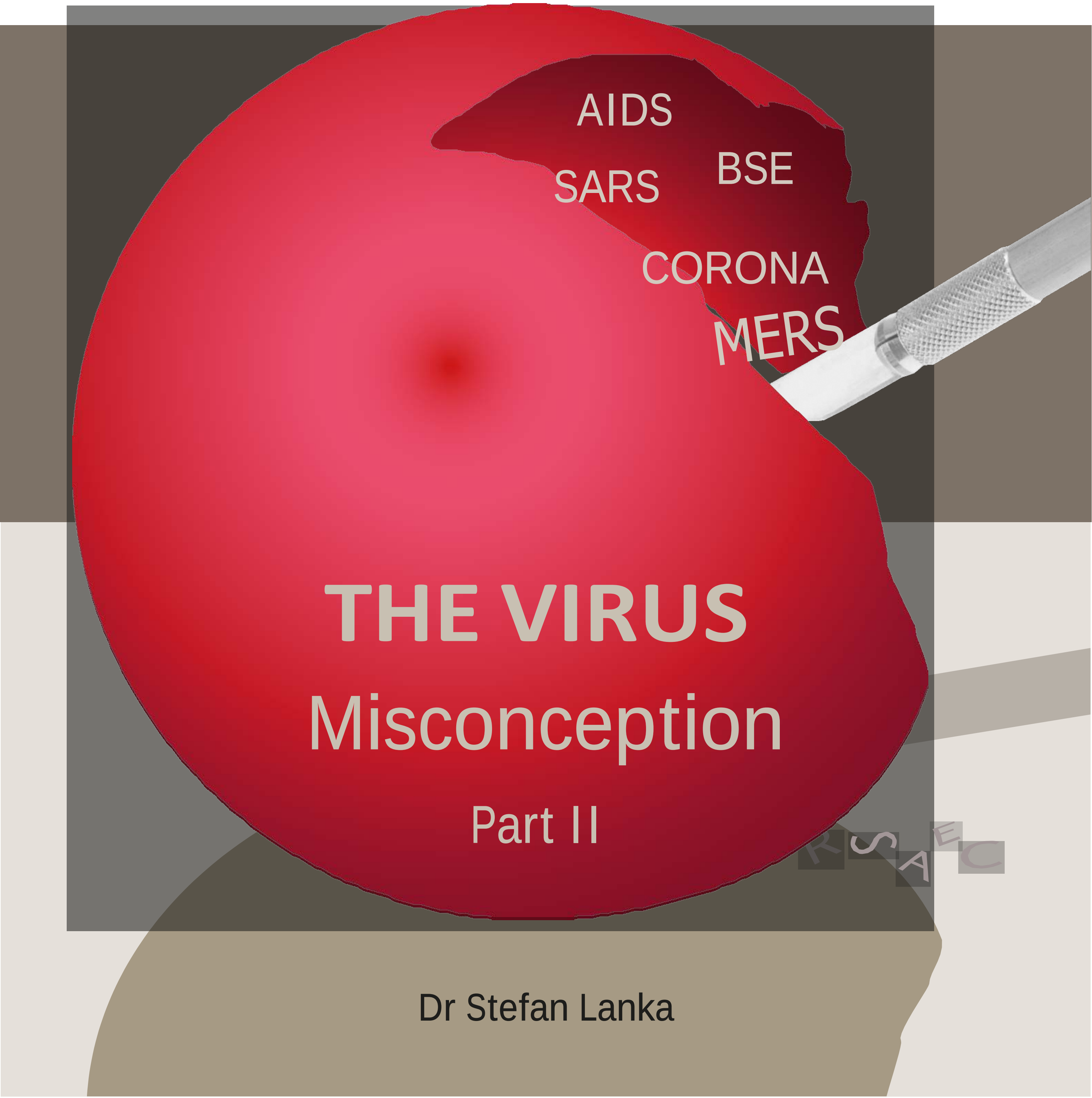

THE VIRUS

Misconception

Part II

Dr Stefan Lanka

The Virus Misconception Part II

The beginning and the end of the corona crisis

Dr. Stefan Lanka

According to the definition of SARS and of Corona or Covid-19, atypical pneumonia is considered to be the characteristic clinical picture of the illness. If pathogens commonly associated with the disease are proved to be present, the pneumonia is classified as typical, if not, pneumonia is classified as atypical. A decisive fact in the SARS and Corona-crisis is that at least 20-30% of all diagnosed pneumonias are classified as atypical. The causes of atypical pneumonia are clearly known and therefore they should NOT be ascribed to an unknown virus.

This knowledge is suppressed or disregarded by infectiologists and virologists and it is the basis *of the current state of fear and panic, as the impression spreads among the affected people, the public opinion and among politicians that atypical pneumonia is especially dangerous and deadly due to the lack of drugs or vaccines for the supposedly new illness.*

As soon as the test method for the detection of the supposed new virus was launched, the involved parties conceal the fact that healthy people test "positive" as well, the so-called asymptomatic carriers, which automatically leads to an increase in the number of cases.

First, patients with typical pneumonia are recorded as having contracted the virus and then more and more people with other illnesses join the list. This is regarded as practical evidence of the virus propagation. New medical conditions are added to the original "atypical pneumonia", comprising a so-called "syndrome" that is presented as the "new viral illness".

The other decisive fact — not just for SARS or the corona crisis — is that virologists, by assuming the existence of pathogenic viruses, suppress for understandable reasons an underlying truth. The current testing method tests for the presence of a specific genetic material. However, the genetic sequences used as a “template” for such tests have not been isolated from a virus. Scientists isolate typical genetic sequences released by dying cells and tissues. These generally short genetic sequences, components of human metabolic processes, are the foundation of the subsequent laboratory work. With the help of computer programs, virologists “conceptually” construct a longer RNA or DNA strand out of the many isolated shorter genetic sequences. These constructed RNA or DNA strands are then claimed to be real viral strands. That is the reason why so many healthy people end up testing positive again and again.

To overcome a crucial contradiction, virologists consequently disregard two prescribed rules of good science. The first one is that scientists need to verify all claims themselves. The second one is that all assumptions and methods need to be verified by means of control experiments. If they carried out the control experiments, they would realize that ALL short genetic sequences that are conceptually combined to form a viral genetic strand are in reality products of the human metabolism and do not come from a supposedly external virus.

The momentum of the Corona crisis was triggered once a message written on 30 December 2019 by a young Chinese ophthalmologist leaked on the internet. In this quickly spreading message he was informing some of his friends about the fact that several people had been put into quarantine at his hospital and that at least seven of them had tested positive for SARS. He advised them to be *careful and protect themselves. Prof Christian Drosten, head of the Institute of Virology at the Charité – Medical School in Berlin, was informed about the situation and he immediately started to develop a test for SARS viruses despite the fact that, by that date, the news from China about a supposedly SARS outbreak were not confirmed and the Chinese virologists had not even published their investigations.*

The Chinese virologists of the Chinese Center for Disease Control and Prevention (abbreviated as CCDC) published their first results on 24 January 2020 and on 3 February 2020, respectively. They reported about the isolation of many short genetic sequences that, when conceptually arrayed, could represent the genome of a new virus. These authors -and also other virologists involved until today- specifically indicated that the necessary experiments, required to conclude that these genetic sequences actually *belonged to a pathogenic virus, had not been carried out. On the contrary: the Chinese virologists claimed that the constructed genetic strand showed a 90% similarity to other genetic strands ascribed to harmless corona viruses which had been found in bats decades ago.*

As early as 21 January 2020 (3 days before the first publication of the CCDC!), the WHO recommended that all countries use the testing method developed by Prof Drosten. As we will see later on, his claim to have developed a reliable detection test for the virus that was supposedly spreading in China greatly aggravated and globalized the panic around the pandemic and he did this while ignoring the obligatory rules of conduct for scientific research, which are an integral part of his work contract, and by violating the logic and general principles of virology.

1. The beginning of the corona crisis

On 30 December 2019 in Wuhan, the young ophthalmologist Li Wenliang contacted seven other fellow physicians through the WeChat app to inform them that, at his hospital, several people had been put into quarantine and that seven of them were allegedly infected with the SARS virus. It had not been his intention to unleash a wave of panic, he just wanted to alert his friends and to recommend them to take protective measures. Otherwise he would have published this information on the internet on his own. However, one of the seven receivers of this message ended up publishing a screenshot of the conversation on the internet without being aware of the consequences. The news spread rapidly inside China and overseas.

This leak unleashed a wave of fear and panic in China and a huge amount of information requests were sent to the government and to the health authorities. The memory of the 2003 SARS virus crisis, which the World Health Organization (WHO) had classified as a “global threat” on 12 March 2003, was still fresh in the minds of the Chinese citizens. The government reacted quickly and a “rapid reaction group” of epidemiologists and virologists of the CCDC was sent to Wuhan on 31 December 2019 in order to assist the health authorities of the city and the surrounding region. Their mission was to test and verify the assumption that an outbreak had indeed taken place. Provided that this had been the case, they were expected to bring the situation under control.

The first publication of the authors of the CCDC regarding the results of their preliminary investigation, published under the title “A Novel Coronavirus from Patients with Pneumonia in China”[1], does not mention any increase in the number of atypical pneumonia cases (“patients with pneumonia of unknown cause”). What the report highlights is one common characteristic shared by a cluster of affected patients. What they had in common was the regular visit to the Huanan Seafood Wholesale Market in Wuhan. The group of patients affected by the atypical pneumonia was certainly small, as the CCDC workers took swab and fluid samples of the lower respiratory tract from only four people in order to look for any known or unknown pathogens.

In the meantime, panic was taking over Wuhan and its surroundings. On 3 January 2020, the police had the ophthalmologist Li Wenliang sign a gag order forcing him to remain silent and to abstain from further “spreading rumors” about the possible SARS outbreak. This measure, however, did little to slow down the panic. The situation became more tense when, on 10 January 2020, Li Wenliang developed symptoms of pneumonia along with his parents. Wenliang isolated himself with the conviction that he had “caught” the SARS virus from a patient the day before. This increased the panic as well.

The physicians who were looking after him tried several testing methods available, but Li Wenliang tested negative to all of them. His health worsened by the day on par with an increasing media coverage and an increasing public interest in his fate. More tests were carried out until he finally tested positive for SARS on 30 January 2020. The SARS panic escalated to new heights and the way was paved for the oncoming global corona crisis.

Li Wenliang made this [positive] result available to the public on the internet with the following words: “Today nucleic acid testing came back with a positive result, the dust has settled, finally diagnosed.“

This message aggravated the already existing panic. The last straw that broke the camel’s back was the leaking to the public of the gag order signed by Wenliang on the 3 January 2020. For many people this was a clear evidence that the Chinese government was hiding a SARS outbreak and that the young physician, despite being ill and despite being under threat, courageously tried to inform the public. His health deteriorated further, the intensive use of antibiotics proved ineffective and he eventually died on 7 February 2020. The situation was on the brink of escalation due to the chaotic and contradictory way in which the government informed about his death. This was and remains the central foundation that led the Chinese and international public opinion to assume that a new SARS outbreak had taken place in Wuhan. The name was eventually changed to Covid-19 and classified as a pandemic.

2. One of the two possible causes of Li Wenliang's fear

Li Wenliang's fear was based on the events of 2003. Back then, several Western scientists were studying an increase in the number of atypical pneumonia cases in Southern China. Two days after Prof Drosten's participation in the conceptual construction of an RNA strand allegedly belonging to a new virus (SARS-CoV-1)[2], the German scientist offered a test for this new virus[3]. Around 800 people with atypical pneumonia (i.e. a pneumonia where no known pathogens were identified) tested positive with it. Most of these people died – probably due to medical malpractice and "overtreatment" – after being diagnosed with SARS instead of "atypical pneumonia".

The reason why the fear of SARS perpetuated across time and was still present in 2019 can be traced back to two scientific papers published in 2013[4] and 2014[5]. These publications set in all kinds of speculations about the fact that new SARS Corona virus outbreaks were a matter of time. The authors of both papers claim that there is evidence of the presence of short genetic sequences in healthy bats that might be classified as components of a virus. These short genetic sequences were said to be similar to the genetic sequences that in 2003 were declared as constituents of the alleged SARS-CoV-1 (SARS Coronavirus 1). SARS stands for Severe Acute Respiratory Syndrome, which is a description of the symptoms of an atypical pneumonia.

The conceptual construction of this fictious viral genetic material is presented as if it existed and could represent a real virus. Their claim is that such a harmless virus, present in bats and other animals, could be transmitted to humans by means of bites, contact or consumption and would pose a deadly threat. Once inside the human body, the virus would be able to mutate into a pathogenic new SARS corona virus.

The authors considered such an incident and the resulting wave of virus-related illnesses, e.g. atypical pneumonia, to be inevitable.

Virologists have not been able up to this day to isolate a SARS virus from any patient, bat or any other wild animal in order to determine a complete and intact genetic strand belonging to a SARS virus, in other words, in order to determine the genome of the virus. Their assumption of the existence of viral genetic strands with an identical structure to the ones that they conceptually construct out of the isolated shorter genetic sequences has not been proved. Although there are very simple techniques available that enable the determination of the length of genetic sequences, the existence and presence of a complete viral genetic strand belonging to a SARS virus has never been demonstrated.

These false claims were the basis of Li Wenliang’s fears as well as of the fears of many other physicians and infectiologists beyond Wuhan. It also explains why the efforts of all virologists and epidemiologists working for the CCDC were directed after 31 December 2019 toward finding similar genetic sequences to the ones defined to be components of the 2003 SARS Corona virus (more on this below).

3. The second of the possible causes of Li Wenliang’s fear

Media outlets ignited the SARS and corona crisis once they started disseminating the news of an increase in the reported cases of atypical pneumonia, a claim that was never proven. It was simply assumed from the very beginning that the emergence of cases of atypical pneumonia had to be related to a new virus, because some of the patients had visited meat markets regularly. In order to confirm their hypothesis of an unknown virus causing the atypical pneumonia, many facts described by the medical and scientific literature were suppressed. There is a wide range of causes for atypical pneumonia besides the “infectious” explanation and, for several reasons, this type of pneumonia can end up being deadlier than the so-called “typical” version.

The “non-infectious” causes are, among others, the inhalation of toxic gases, solvents and other chemical products. Things like food, beverages or gastric content getting into the lungs due to swallowing problems or due to unconsciousness can lead to pneumonia (aspiration pneumonia). Even water on its own can cause an acute atypical pneumonia if it gets into the lungs. Other possible causes are associated with immunological disorders responsible for allergies and autoimmune reactions. Cancer treatments by means of radiation are known to cause lung inflammations indistinguishable from those associated with typical pneumonias. Elderly people also suffer from hypostatic pneumonia caused by water retention (oedemas), long periods of bed confinement and heart and/or kidney problems leading to insufficient aeration and irrigation of the lungs, inflammation and lastly to an atypical pneumonia.

Obviously, a combination of latent causes can have the same result. If initially no known pathogens are detected and the pneumonia is classified as atypical, it is common that at some point a secondary bacterial focus arises, which changes the classification and the pneumonia becomes “typical”. This is the reason why atypical pneumonias in relation to the typical ones probably amount to more than the 20-

30% share attributed to the former. Simply put, most pneumonias are diagnosed at a later stage when bacteria are already present and not at the beginning, when these bacteria are absent.

The first two publications dealing with the corona virus[6] documented the medical examinations performed on five patients with pneumonia, but any other cause besides the viral explanation was ruled out beforehand. No hint or background information was investigated that might have taken into account the possibility of “non-infectious” causes like the ones that we have briefly mentioned. This is not something that virologists usually consider, and given the climate of panic in Wuhan, the members of the CCDC had no other choice but to look for a pathogenic virus. Focusing on an alleged viral cause influences how patients are going to be treated, as they are exposed to a cocktail of antibiotics with strong side effects that, in case of overdoses, can even kill the them.[7] Extreme panic, especially when dealing with respiratory issues, can cause death all by itself, with no other causes. Panic can kill people rapidly, not only those with respiratory and cardiovascular problems.

The answer to the following question is key to put an end to the corona crisis: has a new virus been proved to exist or have the short genetic sequences that are inherent to the human body only been misinterpreted as components of a virus? The perpetrators of the current crisis are already claiming, the way they did during the H1N1 crisis over a decade ago, that the only solution is a vaccine. However, the concept of vaccination has been refuted just like the one about viruses.

A brief reminder of the nowadays forgotten 2009 swine flu pandemic will be very helpful for the assessment of the triggered and maintained corona crisis. Back then, most of the German population was eager to get vaccinated against the supposed virus causing the swine flu. The nationwide mass vaccination project had to be postponed due to the late delivery of the vaccines. Apparently, the vaccines could not be pre-filled in syringes as the adjuvants, that were being used for the first time, would have damaged the vaccine fluid. The proposed solution was to store the vaccine without the adjuvants in vials containing 10 doses and mix both shortly before the vaccination.

A scandal was lurking around the corner. It was eventually made public that the adjuvants, without which the vaccine has no effect whatsoever, had never been tested and to make things worse, that they were made out of nanoparticles. Nanoparticles are known to be very reactive due to their tiny size and they are widely used as catalysators in chemical reactions. Not to mention the fact that the human organism is not able to metabolize or to eliminate these nanoparticles easily. The story reached its climax as soon as the information spread among the public opinion that the chancellor Angela Merkel and the German army would get the same vaccine but without the adjuvants, while the police and the general population would be vaccinated with the vaccine containing nanoparticles that the human body cannot metabolize and eliminate.

In the end, 93% of the population rejected the vaccine, which was then administered to the other 7%. The overall refusal magically wiped out overnight all references to the virus in the media while the German government was busy burning millions of unused vaccine vials. (I would like to add a little joke: the paranoia surrounding the swine flu H1N1 not only vanished, but also the reports of new infections with it and the corresponding media coverage.

One could conclude that the swine flu virus mutated into a fish flu virus, was then carried away by salmons only to end up in the Wuhan fish market and strike back with a vengeance).

The swine flu pandemic was not planned well enough to ensure massive vaccinations, but this did not prevent all involved epidemiologists, infectiologists and virologists to draw the necessary conclusions. They analyzed the causes and published their conclusions and recommendations for the future in the edition no. 12, dated December 2010, of the German Federal Health Bulletin under the meaningful title “Pandemics, Lessons Learned”. Which basically means: The lessons that we learned from the swine flu H1N1 failure!

Some of the articles included in that edition are available on the internet[8], however the most important ones are not to be found. Thus, the crucial recommendations for the management of a pandemic are the following:

- Making sure that experts do not contradict themselves in public discussions.
- Early involvement of mass and social media.
- Control of the internet. This is to avoid that any statement or criticism weakens the consensus and acceptance of the measures adopted by politicians in the name of society.

These recommendations were meticulously implemented this time. The internet is censored and critics are being kept at bay and discredited. Any argument that challenges the official truth about the pandemic and manages to reach the public opinion … is ignored. In fact, each country has its own government speaker giving the daily update of the corona crisis. In Germany, Prof Drosten is the only chosen authority in the field. The only “criticism” that he had to face came from an HIV virologist and it was so weak that at the end the central statement concerning the existence of a new virus called SARS-CoV-2 was strengthened.

4. The globalization of the Chinese SARS virus panic and how Prof Drosten set the course for the corona crisis

Prof Christian Drosten, head of the Institute of Virology at the Charité Medical School in Berlin, claims to have developed a test since 1 January 2020 that allows the detection of the new corona virus in the human body in a reliable way.[9] The WHO started recommending the use of that test to China and to other nations on 21 January 2020, claiming that the testing method was indeed able to detect the presence of the new corona virus and thus it was able to determine the spreading of the virus.[10]

In order to a) be able to understand the underlying hypothesis and the course of action behind Prof Drosten’s claims and in order to b) verify if his conclusions that he has developed a reliable testing method have been scientifically validated or not, or even if they have been refuted, we require additional explanations. We need to understand the meaning of the terms, the techniques and the details of his argumentation, as well as the two central publications that Prof Drosten is referencing.

- How are viruses and a corona virus defined?
- How are genetic sequences defined in this context?
- How do the detection methods of genetic sequences work that are labeled as PCR, RT-PCR and real-time RT-PCR?
- When can it be concluded that the presence of specific genetic sequences in the human body implies the presence of a virus?

- How is the existence of a virus scientifically demonstrated?

Concepts

- A virus is scientifically defined by its specific genome, which is unique for this virus.
- The genetic material of a virus is also called viral genetic strand, viral genetic molecule or genome (we will use the latter from now on).
- The genome of the virus contains a chain of different genetic sequences, the so-called viral genes, that produce the different viral proteins.
- The nucleic acid of a viral genome can be either RNA or DNA.
- The definition of corona viruses describes them as consisting of an RNA nucleic acid surrounded by a shell or capsid.
- The genome of a specific virus is defined by the exact determination of its length and the structural composition of its DNA or RNA strand.

- The composition of a viral genome results from the precise determination of the number and the specific sequence of the four building blocks that make up its genetic material, i.e. the nucleotides.
- The process for determining the specific sequence of nucleotides is called sequencing.
- The result of determining the sequence of nucleotides of a genome is described as sequence or as genetic sequence.
- Pathogenic viruses are defined as having a unique sequence which is not present in healthy organisms.
- In order to verify and determine the presence of a virus, and following the most fundamental rules of scientific reasoning, the virus needs to be isolated and displayed in its pure form in order to rule out that cellular genetic sequences are misinterpreted as components of a virus.
- The determination of the sequence of a given genetic material is only possible in the

form of a DNA.

- In order to determine the sequence of an RNA genetic material, it needs to be biochemically transformed into DNA first.
- The process of transforming an RNA genetic material into DNA
form is called “reverse transcription”, abbreviated as RT.

The techniques used by Prof Drosten and the first conclusions

· Gel electrophoresis is a reliable standard technique for detecting and determining the presence and length of genomes by dividing the DNA and RNA nucleic molecules lengthwise with the application of an electric current to the gel. The negative and positives charges on both ends make the molecules move through the gel, the larger molecules moving more slowly than the smaller ones, which ends up forming distinct bands on the gel according the size and length of the molecules. In order to determine more easily the length of the nucleic acids under study, nucleic acids with a known length are added for comparison.

· If the concentration of a specific genome is so low that the gel electrophoresis technique is not suitable anymore to determine its presence and size, the technique called polymerase chain reaction (PCR) can rapidly make millions of copies of a very small DNA sample, that is, the PCR can “amplify” a small concentration and make it large enough to be examined. Thanks to this PCR technique, one can obtain enough material for further determination of the length and sequence of the DNA sample.

The inventor of the PCR technique, Karry Mullis, to whom the Nobel Prize was awarded in 1993 for this invention, indicated early on that this method was designed to be used in cleanrooms such as the ones available in semiconductor factories and, above all, that it was prone to error. In his award ceremony speech which can be read on the internet page of the Nobel Prize Committee, Mullis also pointed out that there was no scientific evidence that the genetic material defined as the genome of HIV can cause immunodeficiency or any other of the illnesses which are invalidly grouped under the name of a single illness called “AIDS” and treated with very toxic chemotherapy. He concluded that the theory of “HIV” causing immunodeficiency only arose due to scientific consensus-building.

The amplification of DNA by means of the PCR technique requires the prior knowledge of the composition (i.e. the sequence) of that DNA. A DNA can only be multiplied with the PCR technique if short, artificially produced DNA strands (called primers) are bound to the beginning and the end of the DNA, which exactly correspond to the sequence of the beginning and the end of the DNA to be multiplied. Primers are a small set of nucleotides (24 to 30 bases in length) that are attached at the beginning and at the end of the DNA and delineate the area that will be amplified. In other words, the prerequisite for using the PCR is to know exactly what is going to be amplified.

Once the above information is understood, it is easy to realize that the PCR method cannot detect or identify any unknown sequences or any unknown viruses. Only the prior determination of the sequence of a virus makes it possible for scientists to develop a specific PCR test designed to detect the given genetic sequence that belongs to a virus. In other words, the PCR test requires the preparation of a genetic “template”.

- At the early stages of the PCR technique, it was only possible to determine the amount of amplified DNA with the gel electrophoresis method only after having stopped the PCR amplification process. At present, certain dyes are added to the enzymes and substances required for PCR. The detection of these dyes during the PCR shows roughly what concentrations of artificially replicated DNA were created and roughly how much DNA was actually present at the start of the PCR. Since the amount of artificially generated DNA can be roughly determined while the PCR technique is running, this progress of the PCR technique is referred to as “real-time PCR”. A “real-time PCR”, which is preceded by another step, the conversion of RNA into DNA by means of “reverse transcription” (RT), is therefore called “real-time RT PCR”.

- The test that Prof Drosten invented for the detection of the corona virus is a “real-time RT PCR”. On 1 January 2020 he downloaded a database of short genetic sequences theoretically ascribed to the original SARS viruses. On the basis of these short genetic sequences, interpreted as possible constituents of SARS viruses, he developed the “template” for his test, that is, he designed the primers that would delineate the genetic sequences to be amplified by his “real-time RT PCR” test in order to detect the “still” unknown virus in China.

In the meantime, on 10 January 2020 and on 12 January 2020 the first preliminary compilations of genetic sequences related to the virus appeared on the internet, which were subsequently modified and published on 24 January 2020 and on 3 February 2020.[11] These publications represented the first attempts of the Chinese scientists to identify the unknown virus. The CCDC virologists used computer programs to theoretically combine the sequences of short genetic particles into a possible genetic strand. The virologists indicate however in both publications that they lacked the necessary evidences to claim that the proposed sequences could cause diseases. The proposed sequences were still preliminary and were not subjected to the strict processes of scientific review.

The crux of the matter is that the World Health Organization was already recommending on 21 January 2020 the PCR test developed by Drosten, that is, before the first publications of the Chinese experts containing the preliminary virus sequences even came to light on the 24 January 2020 and on the 3 February 2020. Why does all this myriad of dates matter? It shows that Prof Drosten used scientifically untested data for his rapidly globalized PCR test for the detection of the 2019-n CoV. This did not prevent. This did not prevent the rapid expansion of the test which, with the acquiescence of the WHO, was starting to be used everywhere. On 7 February 2020[12], the virus was renamed “SARS-CoV-2” with the cooperation of Prof Drosten.

This name change from “nCoV” to “SARS-CoV-2” gave the impression to the public opinion that the world was not facing a harmless or weak virus, but a pathogenic and very dangerous SARS virus that caused the illness that had killed the Chinese hero Li Wenliang, who had so courageously exposed what the Chinese government was trying to hide. Therefore, Prof Drosten and his colleagues fulfilled the horror scenarios and expectations of the population: “finally diagnosed”. These expectations originated with the wave of panic unleashed by Li Wenliang’s warnings and were endorsed by Drosten. We have to take into account the crucial fact that, at that time, the Chinese virologists involved in the research in Wuhan were pointing out – and they still do at present – that they had no evidence for claiming that the new virus was responsible for causing any illness. What if these genetic sequences under examination were present in some ill people, in healing processes of the body, after these processes, in some or many healthy people or even what if they could potentially show up in all humans?

This alone proves that Prof Drosten has crossed the clearly recognizable line between a scientifically justified action and an obvious and serious fraud. He will be unable to find an excuse by saying that he published his test procedure on January 23, 2020[13] in a scientific magazine which does not check the statements made therein before publishing them.

5. The decisive questions for the end of the corona crisis

We need to ask ourselves if Prof Drosten has fulfilled his scientific duty – essential part of his employment contract[14] – and therefore if he has thoroughly verified all the claims included in his publication about the PCR detection method developed by him and, for that matter, all the public statements that he made in relation to this research.

The questions are the following:

I. Did Prof Drosten verify if the genetic sequences that he used as the basis for the development of his detection test actually come from a virus?

II. Did Prof Drosten carry out the mandatory control experiments to test his hypothesis that the genetic sequences used by him were constituents of a virus? Did he carry out these control experiments in order to rule out the possibility that these genetic sequences, ascribed to an alleged virus, were in reality particles arising during all metabolic processes, even present in plants such as papayas in Tanzania[15] or whose presence in human metabolism is increased during diseases?

III. On the basis of which hypothesis, experiments and control experiments can Prof Drosten conclude that his test is able to "detect" a complete, active and pathogenic virus when this test is only testing for the presence of 2 genes out of the 10 genes that theoretically constitute the genome of the corona virus? How does Drosten know that he is not simply testing for fragments of a virus resulting from a successful "battle" of the immune system or for the presence of "defective", "incomplete" and "harmless" viruses in our genome, that are considered to constitute 50% of the total genes of our chromosomes?

<u>The answers are obtained from the documented actions of Prof Drosten during the</u>

development of his test and from his documented inaction until today.

The virologist Prof Drosten developed the test for the new corona virus (first known as 2019-nCoV and then since 7 February 2020 renamed SARS-CoV-2) and he described its development in a scientific paper that was published on 23 January 2020.[16] On page 3 of this paper, left column and 8th line from below, he describes the first and decisive steps that shaped his course of action: “Before public release of virus sequences from cases of 2019-nCoV, we relied on social media reports announcing detection of a SARS-like virus. We thus assumed that a SARS-related CoV is involved in the outbreak.“

To sum up, Prof Drosten and his colleagues relied on social media to assume that a SARS-related corona virus could be the cause of the atypical pneumonia outbreak. At that time there was no clinical data available that could support such claims. What was his next step?

„We downloaded all complete and partial (if>400 nt) SARS-related virus sequences available in GenBank by 1 January 2020.“ It continues on the right column of the 3rd page, 3rd line from above: “These sequences were aligned [note from the author: by means of a predetermined SARS-virus standard sequence] and the alignment was used for assay design (Supplementary Figure S1). Upon release of the first 2019-nCoV sequence at virological.org, three assays were selected based on how well they matched to the 2019-nCoV genome (Figure 1).

His statements give us clear answers, conclusions and consequences:

I. Did Prof Drosten verify if the genetic sequences that he used as the basis for the development of his detection test actually

come from a virus?
The answer is no! By no means was he able to verify if the genetic sequences that he used for his test originated from a virus and, specifically, if they were related to the alleged virus in China due to the fact that the two Chinese publications dealing with the first clinical results were available only after the market launch of his test.

II. Did Prof Drosten carry out the mandatory control experiments to test his hypothesis that the genetic sequences used by him were constituents of a virus? Did he carry out these control experiments in order to rule out the possibility that these genetic sequences, ascribed to an alleged virus, are in reality particles arising during all metabolic processes, even present in plants or whose presence in human metabolism is increased during diseases?

The answer is no! Neither him nor the Chinese virologists working for the CCDC nor any other virologists have demonstrably carried out these necessary control experiments until today and if the opposite is true, at least they were not published. These experiments require the sequencing of short genetic sequences coming from the metabolism of healthy people. These sequences must undergo the same process than the ones isolated from supposedly infected people and used for the conceptual construction of a viral genetic strand, that is, with the same computer programs, the researchers should try to build a viral genetic strand out the short genetic sequences extracted from healthy people. Such an experiment was either never performed or never published. Even worse, such basic control experiments, which are not only mandatory according to the logic of virology but also necessary to assess experimental results, are not even mentioned. The results of such a control experiment would, on their own, bring the corona crisis to an end.

From a scientific perspective, another obvious control experiment would be to use the PCR method (real-time RT-PCR) to test as many clinical samples as possible coming from people with totally different symptoms and diseases than the ones ascribed to the corona virus, as well as to test clinical samples coming from both healthy people and plants or animals. The aim is to check if these samples also test “positive”. This PCR test is being used millions of times around the world. Control experiments are the only way to assess that this method has any validity, any reliability or any informative value and they are also the only way to make sure that you don’t have millions of cases of misdiagnosis around the world because it is defective and is testing people “positive” for other reasons rather than a virus. These control experiments have not been carried out until today, and no one is even claiming to have carried out such experiments. Maybe that is the reason why the inventors and manufacturers of these tests clearly indicate in their package leaflets that the tests are only suitable for study purposes and not reliable for clinical purposes.

I can forecast with certainty that those people with diseases affecting the ectodermal squamous epithelium tissue, like for example patients with a kidney condition, will test positive with Prof Drosten's PCR method in 100% of the cases as soon as a smear sample is amplified a little and concentrated. There is a high chance that even all organisms can potentially test positive.

I appeal herewith to biochemists, bioinformaticians, virologists and cell culture specialists to encourage them to carry out the aforementioned control experiments, to publish the results and get in touch with me. I

myself have designed a control experiment which discards from the very beginning the possible excuse that the genetic material might become contaminated with SARS-CoV-2 prior or after the control experiment.

The costs of the experiment will be covered in full if I am allowed to be present during the experiment together with some independent observers and if all steps are thoroughly recorded and documented. Please we encourage you to get in touch with us, the contact information is available at the webpage of our publisher. The results will automatically put an end to the corona crisis, however, my own results of such control experiments have to be backed up by those of other scientists.

III. On the basis of which hypothesis, experiments and control experiments can Prof Drosten conclude that his test is able to “detect” a complete, active and pathogenic virus when this test is only testing for the presence of 2 genes out of the 10 genes that theoretically constitute the genome of the corona virus? How does Drosten know that he is not simply testing for fragments of a virus resulting from a successful “battle” of the immune system or for the presence of “defective”, “incomplete” and “harmless” viruses in our genome, that are considered to constitute 50% of the total genes of our chromosomes?

Prof Drosten does not seem to have taken into consideration such logical questions as there is no trace of them in his publications or statements. The detection of short genetic sequences assumed to be constituents of a larger viral genetic strand can never serve as evidence for the presence of a complete virus that is therefore capable of replication. The PCR test does not verify the presence of the complete genome of the alleged virus. It simply verifies the presence of a limited amount of shorter genetic sequences. In order for the PCR test to be considered a valid and reliable detection method, additional research should be undertaken to support the claim that the detection of short genetic sequences, assumed to be fragments of a virus, automatically shows the presence of a whole and intact viral genome. This kind of obvious and logical studies have been neither carried out nor mentioned to date.

Prof Karin Mölling, a leading virologist in the area of cellular particles grouped under the description “endogenous viruses”, also described as harmless, incomplete or defective viruses, considered the measures taken during the corona crisis as unjustified. She showed in her publications and even in a book[17] that half of the human genome, in other words, half of the sequences constituting our chromosomes originate from inactive and defective viruses.

What she does not know, or maybe she is concealing it, is the fact that human metabolism constantly generates a huge amount of RNA genetic sequences of many types and compositions that do not show up in form of DNA sequences in the chromosomes. This fact alone questions any claims concerning the existence of all RNA viruses, such as the corona viruses, Ebola viruses, HIV, the measles virus and the SARS viruses.

This fact is also the reason why carrying out the control experiments that we proposed would not only bring the corona crisis to an end, but also the fear and medical malpractice caused by the science of virology dealing with alleged pathogenic viruses. I can assure that the real causes and phenomena of infection ascribed to viruses have a scientific explanation, in the positive meaning of the word “scientific”. I refer therefore to my previous article “The Virus Misconception Part I” published in

German in the magazine WissenschafftPlus Nr. 1/2020 and which can be purchased in PDF format. Naturally, I also refer to the many other previous articles in the magazine dealing with this question.

Continuation of this article will follow.

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14 §2 Grundsätze Guter Wissenschaftlicher Praxis: (1) u.a. „alle Ergebnisse konsequent selbst anzuzweifeln“ und „die anerkannten Grundsätze wissenschaftlicher Arbeit in den

einzelnen Disziplinen einzuhalten.“ (Principles of Good Scientific Practice: (1) amongst others “to question all results consequently” and “to observe the fundamental principles of scientific work as recognized in the individual scientific disciplines”) in: Neufassung der Satzung der Charité Universitätsmedizin Berlin zur Sicherung Guter Wissenschaftlicher Praxis (Revised version of the statutes of the Charité – University Medicine Berlin for ensuring good scientific practice) published June 20,2012 (AMB Charité Nr. 092, S. 658) available here in German: https://www.charite.de/fileadmin/user_upload/portal/charite/presse/publikationen/amtl-mitteilungsblatt/2016/AMB_208.pdf

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16 Ver 9

17 See the book by Karin Mölling published under the interesting title “Viruses: More Friends Than Foes“, 420 pages, published in 2016 in German language.